

1    **Genome Announcement**

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3    **Draft genome sequence of the electricity producing**

4    ***Thermincola potens* strain JR**

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24 **Abstract**

25 *Thermincola potens* strain JR is one of the first Gram-positive dissimilatory metal  
26 reducing bacteria (DMRB) for which there is a draft genome sequence. Consistent with  
27 the physiology of this organism, preliminary annotation revealed an abundance of multi-  
28 heme c-type cytochromes that are putatively associated with the periplasm and cell  
29 surface in a Gram-positive bacterium. Here we report the draft genome sequence of strain  
30 JR.

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46        *Thermincola potens* strain JR, a Gram-positive anaerobe isolated from a  
47        thermophilic microbial fuel cell (MFC), constituted a dominant member of the current-  
48        producing bacterial community (11). Strain JR is a *Thermincola* species in the  
49        Firmicutes belonging to the Peptococcaceae, in the order Clostridiales. It shares 99% 16S  
50        rRNA gene sequence identity with the two known *Thermincola* members, *T.*  
51        *carboxydophilia* and *T. ferriacetica* (9, 13). This strain coupled acetate oxidation to  
52        reduction of the insoluble electron acceptors MFC anodes and hydrous ferric oxide  
53        (HFO) (11). Strain JR is also capable of growth with CO as the sole electron donor and  
54        carbon source.

55        This Firmicutes is the first MFC isolate and *Thermincola* species to be genome  
56        sequenced and is one of only a few genome sequenced *Peptococcaceae* (6, 12). Genomic  
57        analysis will aid elucidation of electron transfer mechanisms by JR, contributing to the  
58        knowledge of extracellular respiration by Gram-positive bacteria. By comparing these  
59        mechanisms to Gram-negative organisms the conserved and disparate aspects of this  
60        seminal metabolism can be identified. This will include analysis of the c-type  
61        cytochromes makeup of the genome, especially the heightened number of proteins with  
62        double heme (CXXCH) motifs and multiple heme binding domains compared to nearest  
63        phylogenetic neighbors with sequenced genomes (5, 7, 8). C-type cytochromes are  
64        essential for the reduction of insoluble electron acceptors by model Gram-negative  
65        bacteria such as *Geobacter* or *Shewanella* species (4, 10), however their role in Gram-  
66        positive mineral respiration is still unknown.

67        JGI sequencing used a combination of 454 and Illumina techniques with 27x  
68        coverage. All library construction and sequencing techniques are available at

69     <http://www.jgi.doe.gov/>. Illumina reads were assembled into 121 contigs using Velvet  
70     0.7.1.18 (14) and shredded into 1Kb pseudo-reads (with 100 bp overlap). The  
71     pseudoreads were incorporated into a hybrid 454/Illumina assembly using the parallel  
72     Phrap assembler ([www.phrap.com](http://www.phrap.com)) (1, 2). Mis-assemblies were corrected with  
73     Dupfinisher (3). Gene modeling was performed using Prodigal (<http://prodigal.ornl.gov/>)  
74     and resulting protein translations were assigned by comparisons to Pfam, KEGG, and  
75     COGs databases using BLASTP or HMMER. The draft genome was a single circular  
76     chromosome of approximately 3036819 bp with an average G+C content of 45.9 %. A  
77     total of 2963 protein-encoding genes were predicted and 393 (6.9 %) had no similarity to  
78     public database sequences.

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80     **Nucleotide sequence accession numbers.** The genome sequence of *Thermincola potens*  
81     strain JR reported in this paper has been deposited in the GenBank database, accession  
82     number: NC\_014152.

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